

#7

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/668,482

DATE: 08/30/2001

TIME: 15:04:31

Input Set : N:\Crf3\RULE60\09668482.txt

Output Set: N:\CRF3\08302001\I668482.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Petkovich, P. Martin, White, Jay A.,
6 Beckett, Barbara R., Jones, Glenville

8 (ii) TITLE OF INVENTION: Retinoid Metabolizing Protein

10 (iii) NUMBER OF SEQUENCES: 43

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Blake, Cassels & Graydon

14 (B) STREET: Box 25, Commerce Court West

15 (C) CITY: Toronto

16 (D) STATE: Ontario

17 (E) COUNTRY: Canada

18 (F) ZIP: M5L 1A9

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage

22 (B) COMPUTER: COMPAQ, IBM PC compatible

23 (C) OPERATING SYSTEM: MS-DOS 5.1

24 (D) SOFTWARE: WORD PERFECT

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/668,482

C--> 28 (B) FILING DATE: 25-Sep-2000

30 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 08/882,164

34 (B) FILING DATE: June 25, 1997

35 (A) APPLICATION NUMBER: 08/667,546

36 (B) FILING DATE: June 21, 1996

37 (A) APPLICATION NUMBER: 08/724,466

38 (B) FILING DATE: October 1, 1996

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Hunt, John C.

42 (B) REGISTRATION NUMBER: 36,424

43 (C) REFERENCE/DOCKET NUMBER: 50767/00010

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: (416) 863-4344

47 (B) TELEFAX: (416) 863-2653

50 (2) INFORMATION FOR SEQ ID NO: 1

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 337 base pairs

53 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

59	TGCCAGTGGG	CAATCTCCCT	ACCAAATTCA	CTAGTTATGT	CCAGAAATTA	GCCTAAACCG	60
61	GAGCCTTTGT	ACATATGTTT	TTATTTTAGA	TGAAGTGTGA	TGTATTGGAT	ATTTTCTAAT	120
63	TTGTTTATAT	AAAGCAGATG	TGTATATAAG	TCTATGCGAA	GAAGCGAAAA	CGAGGGCACT	180
65	ACTTTCTCAT	GGATCACTGT	AATGCTACAG	AGTGTCTGTG	ATGTATATTT	ATAATGTAGT	240
67	TGTGTCATAT	AGCTTTTGTA	CTGTATGCAA	CTTATTTAAC	TCGCTCTTTA	TCTCATGGGT	300

ENTERED

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69 TTTATTTAAT AAAACATGTT CTTACAAAAA AAAAAAA
72 (2) INFORMATION FOR SEQ ID NO: 2
73     (i) SEQUENCE CHARACTERISTICS:
74         (A) LENGTH: 492 amino acids
75         (B) TYPE: amino acid
76         (C) STRANDEDNESS: single
77         (D) TOPOLOGY: linear
79     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2
81 Met Gly Leu Tyr Thr Leu Met Val Thr Phe Leu Cys Thr Ile Val Leu
82 1          5          10          15
84 Pro Val Leu Leu Phe Leu Ala Ala Val Lys Leu Trp Glu Met Leu Met
85          20          25          30
87 Ile Arg Arg Val Asp Pro Asn Cys Arg Ser Pro Leu Pro Pro Gly Thr
88          35          40          45
90 Met Gly Leu Pro Phe Ile Gly Glu Thr Leu Gln Leu Ile Leu Gln Arg
91          50          55          60
93 Arg Lys Phe Leu Arg Met Lys Arg Gln Lys Tyr Gly Cys Ile Tyr Lys
94 65          70          75          80
96 Thr His Leu Phe Gly Asn Pro Thr Val Arg Val Met Gly Ala Asp Asn
97          85          90          95
99 Val Arg Gln Ile Leu Leu Gly Glu His Lys Leu Val Ser Val Gln Trp
100         100         105         110
102 Pro Ala Ser Val Arg Thr Ile Leu Gly Ser Asp Thr Leu Ser Asn Val
103         115         120         125
105 His Gly Val Gln His Lys Asn Lys Lys Lys Ala Ile Met Arg Ala Phe
106         130         135         140
108 Ser Arg Asp Ala Leu Glu His Tyr Ile Pro Val Ile Gln Gln Glu Val
109 145         150         155         160
111 Lys Ser Ala Ile Gln Glu Trp Leu Gln Lys Asp Ser Cys Val Leu Val
112         165         170         175
114 Tyr Pro Glu Met Lys Lys Leu Met Phe Arg Ile Ala Met Arg Ile Leu
115         180         185         190
117 Leu Gly Phe Glu Pro Glu Gln Ile Lys Thr Asp Glu Gln Glu Leu Val
118         195         200         205
120 Glu Ala Phe Glu Glu Met Ile Lys Asn Leu Phe Ser Leu Pro Ile Asp
121         210         215         220
123 Val Pro Phe Ser Gly Leu Tyr Arg Gly Leu Arg Ala Arg Asn Phe Ile
124 225         230         235         240
126 His Ser Lys Ile Glu Glu Asn Ile Arg Lys Lys Ile Gln Asp Asp Asp
127         245         250         255
129 Asn Glu Asn Glu Gln Lys Tyr Lys Asp Ala Leu Gln Leu Leu Ile Glu
130         260         265         270
132 Asn Ser Arg Arg Ser Asp Glu Pro Phe Ser Leu Gln Ala Met Lys Glu
133         275         280         285
135 Ala Ala Thr Glu Leu Leu Phe Gly Gly His Glu Thr Thr Ala Ser Thr
136         290         295         300
138 Ala Thr Ser Leu Val Met Phe Leu Gly Leu Asn Thr Glu Val Val Gln
139 305         310         315         320
141 Lys Val Arg Glu Glu Val Gln Glu Lys Val Glu Met Gly Met Tyr Thr

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142          325          330          335
144 Pro Gly Lys Gly Leu Ser Met Glu Leu Leu Asp Gln Leu Lys Tyr Thr
145          340          345          350
147 Gly Cys Val Ile Lys Glu Thr Leu Arg Ile Asn Pro Pro Val Pro Gly
148          355          360          365
150 Gly Phe Arg Val Ala Leu Lys Thr Phe Glu Leu Asn Gly Tyr Gln Ile
151          370          375          380
153 Pro Lys Gly Trp Asn Val Ile Tyr Ser Ile Cys Asp Thr His Asp Val
154 385          390          395          400
156 Ala Asp Val Phe Pro Asn Lys Glu Glu Phe Gln Pro Glu Arg Phe Met
157          405          410          415
159 Ser Lys Gly Leu Glu Asp Gly Ser Arg Phe Asn Tyr Ile Pro Phe Gly
160          420          425          430
162 Gly Gly Ser Arg Met Cys Val Gly Lys Glu Phe Ala Lys Val Leu Leu
163          435          440          445
165 Lys Ile Phe Leu Val Glu Leu Thr Gln His Cys Asn Trp Ile Leu Ser
166          450          455          460
168 Asn Gly Pro Pro Thr Met Lys Thr Gly Pro Thr Ile Tyr Pro Val Asp
169 465          470          475          480
171 Asn Leu Pro Thr Lys Phe Thr Ser Tyr Val Arg Asn
172          485          490
175 (2) INFORMATION FOR SEQ ID NO: 3
176 (i) SEQUENCE CHARACTERISTICS:
177 (A) LENGTH: 1850 base pairs
178 (B) TYPE: nucleic acid
179 (C) STRANDEDNESS: single
180 (D) TOPOLOGY: linear
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3
184 TGTCGCCGTT GCTGTCGGTT GCTGTCGGAC GCTGTCTCCT CTCCAGAAGC TTGTTTTTCG 60
186 TTTTGGCGAT CAGTTGCGCG CTTCAAC ATG GGG CTG TAC ACC CTT ATG GTC ACC 114
187 Met Gly Leu Tyr Thr Leu Met Val Thr
188 1 5
190 TTT CTC TGC ACC ATC GTG CTA CCC GTT TTA CTC TTT CTC GCC GCG GTG 162
191 Phe Leu Cys Thr Ile Val Leu Pro Val Leu Leu Phe Leu Ala Ala Val
192 10 15 20 25
194 AAG TTG TGG GAG ATG TTA ATG ATC CGA CGA GTC GAT CCG AAC TGC AGA 210
195 Lys Leu Trp Glu Met Leu Met Ile Arg Arg Val Asp Pro Asn Cys Arg
196 30 35 40
198 AGT CCT CTA CCG CCA GGT ACC ATG GGC TTG CCG TTC ATT GGA GAA ACG 258
199 Ser Pro Leu Pro Pro Gly Thr Met Gly Leu Pro Phe Ile Gly Glu Thr
200 45 50 55
202 CTC CAG CTG ATC CTC CAG AGA AGG AAG TTT CTG CGC ATG AAA CGG CAG 306
203 Leu Gln Leu Ile Leu Gln Arg Arg Lys Phe Leu Arg Met Lys Arg Gln
204 60 65 70
206 AAA TAC GGG TGC ATC TAC AAG ACG CAC CTC TTC GGG AAC CCG ACT GTC 354
207 Lys Tyr Gly Cys Ile Tyr Lys Thr His Leu Phe Gly Asn Pro Thr Val
208 75 80 85
210 AGG GTG ATG GGA GCT GAT AAT GTG AGG CAG ATT CTG CTG GGC GAA CAC 402
211 Arg Val Met Gly Ala Asp Asn Val Arg Gln Ile Leu Leu Gly Glu His

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212	90		95		100		105		
214	AAG	CTG	GTG	TCT	GTT	CAG	TGG	CCA	GCA
215	Lys	Leu	Val	Ser	Val	Gln	Trp	Pro	Ala
216					110			115	
218	TCT	GAC	ACC	CTC	TCC	AAT	GTC	CAT	GGA
219	Ser	Asp	Thr	Leu	Ser	Asn	Val	His	Gly
220				125				130	
222	AAG	GCC	ATT	ATG	AGG	GCG	TTC	TCT	CGA
223	Lys	Ala	Ile	Met	Arg	Ala	Phe	Ser	Arg
224			140					145	
226	CCC	GTG	ATC	CAG	CAG	GAG	GTG	AAG	AGC
227	Pro	Val	Ile	Gln	Gln	Glu	Val	Lys	Ser
228			155					160	
230	AAA	GAC	TCC	TGC	GTG	CTG	GTT	TAT	CCA
231	Lys	Asp	Ser	Cys	Val	Leu	Val	Tyr	Pro
232	170				175			180	
234	CGG	ATA	GCT	ATG	AGA	ATC	CTG	CTT	GGT
235	Arg	Ile	Ala	Met	Arg	Ile	Leu	Leu	Gly
236				190				195	
238	ACG	GAC	GAG	CAA	GAA	CTG	GTG	GAA	GCT
239	Thr	Asp	Glu	Gln	Glu	Leu	Val	Glu	Ala
240				205				210	
242	TTG	TTC	TCC	TTG	CCA	ATC	GAC	GTT	CCT
243	Leu	Phe	Ser	Leu	Pro	Ile	Asp	Val	Pro
244			220					225	
246	TTG	AGG	GCA	CGC	AAT	TTC	ATT	CAC	TCC
247	Leu	Arg	Ala	Arg	Asn	Phe	Ile	His	Ser
248			235					240	
250	AAG	AAA	ATT	CAA	GAT	GAC	GAC	AAT	GAA
251	Lys	Lys	Ile	Gln	Asp	Asp	Asp	Asn	Glu
252	250				255			260	
254	GCC	CTT	CAG	CTG	TTG	ATC	GAG	AAC	AGC
255	Ala	Leu	Gln	Leu	Ile	Glu	Asn	Ser	Arg
256				270				275	
258	AGT	TTG	CAG	GCG	ATG	AAA	GAA	GCA	GCT
259	Ser	Leu	Gln	Ala	Met	Lys	Glu	Ala	Ala
260				285				290	
262	CAT	GAA	ACC	ACC	GCC	AGC	ACT	GCA	ACC
263	His	Glu	Thr	Thr	Ala	Ser	Thr	Ala	Thr
264			300					305	
266	CTG	AAC	ACA	GAA	GTG	GTG	CAG	AAG	GTC
267	Leu	Asn	Thr	Glu	Val	Val	Gln	Lys	Val
268			315					320	
270	GTT	GAA	ATG	GGC	ATG	TAT	ACA	CCT	GGA
271	Val	Glu	Met	Gly	Met	Tyr	Thr	Pro	Gly
272	330				335			340	
274	TTG	GAC	CAG	CTG	AAG	TAC	ACT	GGA	TGT
275	Leu	Asp	Gln	Leu	Lys	Tyr	Thr	Gly	Cys
276				350				355	

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278 ATC AAC CCT CCT GTT CCC GGA GGA TTC AGA GTC GCA CTC AAA ACC TTT      1218
279 Ile Asn Pro Pro Val Pro Gly Gly Phe Arg Val Ala Leu Lys Thr Phe
280          365          370          375
282 GAA TTG AAT GGT TAC CAA ATT CCT AAA GGA TGG AAC GTC ATT TAC AGC      1266
283 Glu Leu Asn Gly Tyr Gln Ile Pro Lys Gly Trp Asn Val Ile Tyr Ser
284          380          385          390
286 ATC TGT GAC ACG CAC GAT GTG GCC GAC GTC TTT CCA AAC AAA GAG GAG      1314
287 Ile Cys Asp Thr His Asp Val Ala Asp Val Phe Pro Asn Lys Glu Glu
288          395          400          405
290 TTC CAG CCG GAG AGA TTC ATG AGC AAA GGT CTG GAG GAC GGG TCC AGG      1362
291 Phe Gln Pro Glu Arg Phe Met Ser Lys Gly Leu Glu Asp Gly Ser Arg
292 410          415          420          425
294 TTT AAC TAC ATC CCC TTC GGA GGA GGA TCC AGG ATG TGT GTG GGC AAA      1410
295 Phe Asn Tyr Ile Pro Phe Gly Gly Gly Ser Arg Met Cys Val Gly Lys
296          430          435          440
298 GAG TTC GCC AAA GTG TTA CTC AAG ATC TTT TTA GTT GAG TTA ACG CAG      1458
299 Glu Phe Ala Lys Val Leu Leu Lys Ile Phe Leu Val Glu Leu Thr Gln
300          445          450          455
302 CAT TGC AAT TGG ATT CTC TCA AAC GGA CCC CCG ACA ATG AAA ACA GGC      1506
303 His Cys Asn Trp Ile Leu Ser Asn Gly Pro Pro Thr Met Lys Thr Gly
304          460          465          470
306 CCG ACT ATT TAC CCA GTG GAC AAT CTC CCT ACC AAA TTC ACT AGT TAT      1554
307 Pro Thr Ile Tyr Pro Val Asp Asn Leu Pro Thr Lys Phe Thr Ser Tyr
308          475          480          485
310 GTC AGA AAT TAGCCTAACC GGAGCTTTGT ACATATGTTT TTATTTTAGA      1603
311 Val Arg Asn
312 490
314 TGAACGTGA TGTATTGGAT ATTTTCTATT TTGTTTATAT AAAGCAGATG TGTATATAAG      1663
316 TCTATGCGAG GAAGCGAAAA CGAGGGCACT ACTTTCTCAT GGATCACTGT AATGCTACAG      1723
318 AGTGTCTGTG ATGTATATTT ATAATGTAGT TGTGTTATAT AGCTTTTGTA CTGTATGCAA      1783
320 CTTATTTAAC TCGCTCTTTA TCTCATGGGT TTTATTTAAT AAAACATGTT CTTACAAAAA      1843
322 AAAAAAA      1850
325 (2) INFORMATION FOR SEQ ID NO: 4
326 (i) SEQUENCE CHARACTERISTICS:
327 (A) LENGTH: 497 amino acids
328 (B) TYPE: amino acid
329 (C) STRANDEDNESS: single
330 (D) TOPOLOGY: linear
332 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4
334 Met Gly Leu Pro Ala Leu Leu Ala Ser Ala Leu Cys Thr Phe Val Leu
335 1          5          10          15
337 Pro Leu Leu Leu Phe Leu Ala Ala Ile Lys Leu Trp Asp Leu Tyr Cys
338          20          25          30
340 Val Ser Gly Arg Asp Arg Ser Cys Ala Leu Pro Leu Pro Pro Gly Thr
341          35          40          45
343 Met Gly Phe Pro Phe Phe Gly Glu Thr Leu Gln Met Val Leu Gln Arg
344          50          55          60
346 Arg Lys Phe Leu Gln Met Lys Arg Arg Lys Tyr Gly Phe Ile Tyr Lys
347 65          70          75          80

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VERIFICATION SUMMARY

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]